Amendments to the Specification:

Please replace Figures 1-2 with replacement Figures 1-2 attached hereto as **Exhibit 1** (4 sheets).

Please add the Sequence Listing attached hereto both as **Exhibit 2** (3 pages) and in computer readable form on floppy disk as the Sequence Listing for the subject application.

On page 31, please amend the paragraph at lines 11-12 as follows.

- Figure 1 shows the amino acid sequence for some minimal sequences for starch binding domains suitable for use in the invention; *B. circulans* (SEQ ID NO:1), *A. niger* (SEQ ID NO:2), *T. thermosulfurigenes* (SEQ ID NO:3), *B stearothermophilus* (SEQ ID NO:4).

On page 36, please amend the paragraph at lines 28-31 as follows.

In addition, WT potato plants can be transformed with ~~with~~ a gene encoding a single SBD or a double SBD to determine the competition ~~epompetition~~ between GBSS I and SBD(s) *in vivo*. This may also serve as an alternative way to make an amylose- free potato starch.

On page 37, please amend the paragraph at lines 25-30 as follows.

Additional branching compared ~~comparwed~~ to these reference tests might be achieved when glgB is specifically targeted to (and thus concentrated at) the granule surface by equipping the enzyme with a SBD, i.e. by expressing it *in planta* as a fusion of the invention. In this way, with a fusion of the invention, possibly a larger increase in

branching can be obtained (i.e. compared to transforming with glgB per se), to provide improved freeze-thaw stability of starch solutions.

On page 39, please amend the paragraph at lines 1-19 as follows.

Briefly, the assembly of all constructs for potato transformation was started with the vector pBINI9^{PTT} (Fig. 2A), which already contained the tuber- specific GBSS I promoter, the amyloplast-targeting signal of potato GBSS 1, and the NOS terminator sequence (for legend see figure). The starch-binding modules SBD and GBSS were obtained by standard PCR using the cyclodextrin glycosyltransferase of *Bacillus circulans* and potato granule-bound starch synthase I as a template, respectively. The luciferase template (pLUK07/LUC) was obtained from the North Carolina State University. PCRs were performed in such a way that the appropriate restriction sites were introduced in the genes of interest. The relevant restriction sites are indicated in Figure 2. An artificial linker sequence was designed, containing a BglII and an EcoRl restriction site at, respectively, the 5' and 3' end of the sequence. The amino acid sequence of the PT-rich linker peptide corresponds to "RSPTPTPTTPTPTPTTPTPTPSTE" (SEQ ID NO:5). The correctness of the constructs was confirmed by DNA sequencing. The constructs were introduced in both WT and amylose-free potato plants using standard *Agrobacterium*-mediated transformation procedures. The constructs provide the opportunity (i) to investigate whether SBD and GBSS bind the granule at a different location; (ii) to compare the affinity of SBD, SBD_2 and GBSS for starch during granule biosynthesis; (iii) to verify the concept of targeting foreign catalytic activities to the starch granule during biosynthesis.